

SEQUENCE LISTING

<110> MIYATA, Toshio
KUROKAWA, Kiyoshi

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<141> 2001-10-30

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<212> DNA

<213> Homo sapiens

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Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe
5 10 15

tat gaa gac cag tat ggc gtg gct ctc ttc aac agc atg cgc cat gag 154
Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg His Glu
20 25 30

att gag ggc acg ggg ctg ccg cag gcc cag ctg ctc tgg cgc aag gtg 202
Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg Lys Val
35 40 45 50

cca ctg gac gag cgc atc gtc ttc tcg ggg aac ctc ttc cag cac cag 250
Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln His Gln
55 60 65

gag gac agc aag aag tgg aga aac cgc ttc agc ctc gtg ccc cac aac 298
Glu Asp Ser Lys Lys Trp Arg Asn Arg Phe Ser Leu Val Pro His Asn
70 75 80

tac ggg ctg gtg ctc tac gaa aac aaa gcg gcc tat gag cgg cag gtc 346
Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg Gln Val
85 90 95

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Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu Thr Ser
100 105 110

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gca Ala	aag Lys	tcg Ser	ggc Gly	agt Ser 135	gcc Ala	ccc Pro	atc Ile	ctc Leu	aag Lys 140	tgc Cys	ccc Pro	aca Thr	cag Gln	ttc Phe 145	ccg Pro	490
ctc Leu	atc Ile	ctc Leu	tgg Trp 150	cat His	cct Pro	tat Tyr	gcg Ala	cgt Arg 155	cac His	tac Tyr	tac Tyr	ttc Phe	tgc Cys 160	atg Met	atg Met	538
aca Thr	gaa Glu	gcc Ala 165	gag Glu	cag Gln	gac Asp	aag Lys	tgg Trp 170	cag Gln	gct Ala	gtg Val	ctg Leu	cag Gln 175	gac Asp	tgc Cys	atc Ile	586
cgg Arg 180	cac His	tgc Cys	aac Asn	aat Asn	gga Gly	atc Ile 185	cct Pro	gag Glu	gac Asp	tcc Ser 190	aag Lys	gta Val	gag Glu	ggc Gly	cct Pro	634
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cgg Arg	ctg Leu	aag Lys 245	ggg Gly	aaa Lys	ccg Pro	cag Gln	gag Glu 250	cgg Arg	cag Gln	cgg Arg	cag Gln	tgg Trp 255	atc Ile	cag Gln	atc Ile	826
tcg Ser 260	gac Asp	gcc Ala	gtg Val	tac Tyr	cac His	atg Met 265	gtg Val	tac Tyr	gag Glu	cag Gln	gcc Ala 270	aag Lys	gcg Ala	cgc Arg	ttc Phe	874
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gcc Ala	agc Ser	aag Lys	atc Ile 310	cga Arg	gcc Ala	ttc Phe	atc Ile	ctc Leu 315	ccc Pro	aag Lys	gca Ala	gag Glu	gtg Val 320	tgc Cys	gtg Val	101
cgg Arg	aac Asn	cat His 325	gtc Val	cag Gln	ccc Pro	tac Tyr	atc Ile 330	cca Pro	tcc Ser	atc Ile	ctg Leu 335	gag Glu	gcc Ala	ctg Leu	atg Met	106

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340 345 350	
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Glu Val Thr Asp Met Asn Leu Asn Val Ile Asn Glu Gly Gly Ile Asp	
355 360 365 370	
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Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr His Pro	
375 380 385	
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Leu Lys Met Gln Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg Leu Asp	
390 395 400	
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Gly Leu Gln Gln Arg Phe Asp Val Ser Ser Thr Ser Val Phe Lys Gln	
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cga gcc cag atc cac atg cgg gag caa atg gac aat gcc gtg tat acg	1354
Arg Ala Gln Ile His Met Arg Glu Gln Met Asp Asn Ala Val Tyr Thr	
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Phe Glu Thr Leu Leu His Gln Glu Leu Gly Lys Gly Pro Thr Lys Glu	
435 440 445 450	
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Glu Leu Cys Lys Ser Ile Gln Arg Val Leu Glu Arg Val Leu Lys Lys	
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Tyr Asp Tyr Asp Ser Ser Ser Val Arg Lys Arg Phe Phe Arg Glu Ala	
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485 490 495	
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Cys Lys Ser Glu Leu Pro Arg Phe Gln Glu Leu Ile Phe Glu Asp Phe	
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gcc agg ttc atc ctg gtg gaa aac acg tac gag gag gtg gtg ctg cag	1642
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acc gtc atg aag gac atc ctg cag gct gtg aag gag gcc gcg gtg cag	1690
Thr Val Met Lys Asp Ile Leu Gln Ala Val Lys Glu Ala Ala Val Gln	
535 540 545	
agg aag cac aac ctc tac cgg gac agc atg gtc atg cac aac agc gac	1738
Arg Lys His Asn Leu Tyr Arg Asp Ser Met Val Met His Asn Ser Asp	
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		20					25					30			
His	Glu	Ile	Glu	Gly	Thr	Gly	Leu	Pro	Gln	Ala	Gln	Leu	Leu	Trp	Arg
	35					40					45				
Lys	Val	Pro	Leu	Asp	Glu	Arg	Ile	Val	Phe	Ser	Gly	Asn	Leu	Phe	Gln
	50				55						60				
His	Gln	Glu	Asp	Ser	Lys	Lys	Trp	Arg	Asn	Arg	Phe	Ser	Leu	Val	Pro
65					70				75					80	

His Asn Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg
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Gln Val Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu
100 105 110

Thr Ser Val Asp Gln Tyr Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly
115 120 125

Thr Thr Ala Lys Ser Gly Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln
130 135 140

Phe Pro Leu Ile Leu Trp His Pro Tyr Ala Arg His Tyr Tyr Phe Cys
145 150 155 160

Met Met Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala Val Leu Gln Asp
165 170 175

Cys Ile Arg His Cys Asn Asn Gly Ile Pro Glu Asp Ser Lys Val Glu
180 185 190

Gly Pro Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu
195 200 205

Leu Tyr Gly Thr Trp Glu Met Leu Cys Gly Asn Glu Val Gln Ile Leu
210 215 220

Ser Asn Leu Val Met Glu Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu
225 230 235 240

Gly Pro Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile
245 250 255

Gln Ile Ser Asp Ala Val Tyr His Met Val Tyr Glu Gln Ala Lys Ala
260 265 270

Arg Phe Glu Glu Val Leu Ser Lys Val Gln Gln Val Gln Pro Ala Met
275 280 285

Gln Ala Val Ile Arg Thr Asp Met Asp Gln Ile Ile Thr Ser Lys Glu
290 295 300

Leu Leu Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro Lys Ala Glu Val
305 310 315 320

Cys Val Arg Asn His Val Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala
325 330 335

Leu Met Val Pro Thr Ser Gln Gly Phe Thr Glu Val Arg Asp Val Phe
340 345 350

Phe Lys Glu Val Thr Asp Met Asn Leu Asn Val Ile Asn Glu Gly Gly
355 360 365

Ile Asp Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr
370 375 380

His Pro Leu Lys Met Gln Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg
385 390 395 400

Leu Asp Gly Leu Gln Gln Arg Phe Asp Val Ser Ser Thr Ser Val Phe
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Lys Gln Arg Ala Gln Ile His Met Arg Glu Gln Met Asp Asn Ala Val
420 425 430

Tyr Thr Phe Glu Thr Leu Leu His Gln Glu Leu Gly Lys Gly Pro Thr
435 440 445

Lys Glu Glu Leu Cys Lys Ser Ile Gln Arg Val Leu Glu Arg Val Leu
450 455 460

Lys Lys Tyr Asp Tyr Asp Ser Ser Ser Val Arg Lys Arg Phe Phe Arg
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Glu Ala Leu Leu Gln Ile Ser Ile Pro Phe Leu Leu Lys Lys Leu Ala
485 490 495

Pro Thr Cys Lys Ser Glu Leu Pro Arg Phe Gln Glu Leu Ile Phe Glu
500 505 510

Asp Phe Ala Arg Phe Ile Leu Val Glu Asn Thr Tyr Glu Glu Val Val
515 520 525

Leu Gln Thr Val Met Lys Asp Ile Leu Gln Ala Val Lys Glu Ala Ala
530 535 540

Val Gln Arg Lys His Asn Leu Tyr Arg Asp Ser Met Val Met His Asn
545 550 555 560

Ser Asp Pro Asn Leu His Leu Leu Ala Glu Gly Ala Pro Ile Asp Trp
565 570 575

Gly Glu Glu Tyr Ser Asn Ser Gly Gly Gly Gly Ser Pro Ser Pro Ser
580 585 590

Thr Pro Glu Ser Ala Thr Leu Ser Glu Lys Arg Arg Arg Ala Lys Gln
595 600 605

Val Val Ser Val Val Gln Asp Glu Glu Val Gly Leu Pro Phe Glu Ala
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Ser Pro Glu Ser Pro Pro Pro Ala Ser Pro Asp Gly Val Thr Glu Ile
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Arg Gly Leu Leu Ala Gln Gly Leu Arg Pro Glu Ser Pro Pro Pro Ala
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Gly Pro Leu Leu Asn Gly Ala Pro Ala Gly Glu Ser Pro Gln Pro Lys
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Ala Ala Pro Glu Ala Ser Ser Pro Pro Ala Ser Pro Leu Gln His Leu
675 680 685

Leu Pro Gly Lys Ala Val Asp Leu Gly Pro Pro Lys Pro Ser Asp Gln
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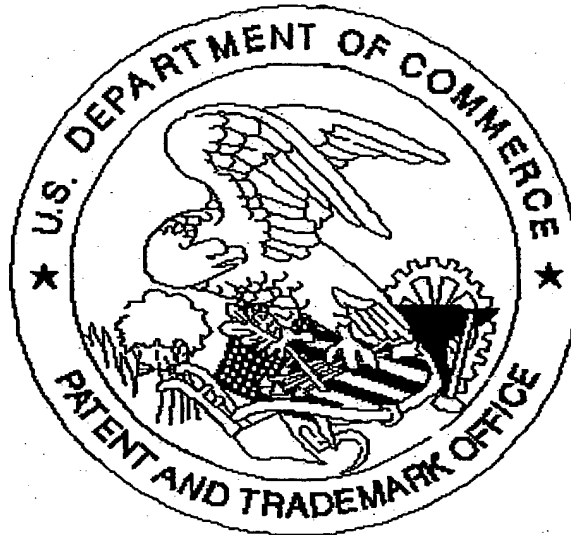
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for scanning. (Document title)

☐ Page(s) _____ of _____ were not
present
for scanning. (Document title)

/ Scanned copy is best available. Figure 2 is very dark